#8

SEQUENCE LISTING

<110> Falco, Saverio Carl
Famodu, Layo
Rafalski, Jan A.
Ramaker, Michael
Tarczynski, Mitchell C.
Thorpe, Catherine

<120> PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING THE METHIONINE CONTENT OF THE SEEDS OF PLANTS

<130> BB-1067-B

<140>
<141>

<150> 08/703,829
<151> 1996-08-27

<160> 55

<170> Microsoft Office 97

<210> 1
<211> 2639
<212> DNA
<213> Zea mays

<400> 1
caccacccac ctcccactcc cagttcaccc cgtcgtcctc ggcgccacca ctcctcgtcc 60
cccggcgcta ctccccccgct ccacggtcca aggaaagatg gcgtcccata ttgttggata 120
ccctcgcatg ggccccaaga gggagctcaa gtttgccttg gagtctttct gggatgggaa 180
gagcagcgcc gaggatttgg agaaagttgc cactgacctg aggtctagca tctggaagca 240
aatgtcagaa gctgggatca agtacattcc cagcaatacc tcgtcgtact acgaccaggt 300
tcttgatacc acggccatgc ttggcgctgt cccagagcgc tactcttgga ctggaggcga 360
gattggcttg agcacctact tctctatggc caggggaaat gccactgtcc ctgccatgga 420
gatgaccaag tggtttgata caaactacca ctttattgtc cctgaacttg gtccaagcac 480
caagttcaca tacgcttctc acaaggctgt ttctgagtac aaggaggcaa aggcgctcgg 540
cattgataca gtcccagtgc ttgttggacc agtctcatac ttgctcctct ctaagcctgc 600
caagggtgtg gagaaatctt tctctcttct ttcacttctt ggtagcattc ttcccatcta 660
caaggaggtt gttgctgagc tgaaggcagc tggtgcttca tggattcagc ttgatgagcc 720
taccccttgtt aaagaccttg atgctcacga attggccgca ttctcttcag catatgctga 780
actggagtca tcgttctctg gattgaatgt gcttatcgag acatacttcg ctgatattcc 840
tgctgagtcc tacaagaccc tcacatcatt gagtggtgtg actgcttacg gtttcgatct 900
tatccgtgga gccaagaccc ttgatcttat caggagcagc ttcccctctg ggaagtacct 960
cttcgctggt gttgtagatg gacgcaacat ttgggctgat gatcttgctg catctcttag 1020
cactcttcat tctcttgagg ctgttgctgg caaggacaaa cttgtggtgt caacctcctg 1080
ctcactgatg cacaccgctg ttgaccttgt aaatgagact aagctggatg atgagattaa 1140
gtcatggctt gcatttgctg cccaaaaggt tgttgaggtt aatgcccttg ccaaggcttt 1200
ggcaggccaa aaggatgagg tctactttgc agccaatgct gctgctcagg cctcaaggag 1260
atcatcgccc agggtgacaa acgaggaggt ccagaaggct gcagctgctt tgaggggatc 1320
tgaccaccgc cgttctacca ctgtttctgc tagattggat gctcagcaga aaaagctcaa 1380
ccttcctgtc cttcccacaa ccacaattgg ttcattccct cagactgtgg aactcaggag 1440
ggttcgccgt gaatacaagg caaagaagat caccgaggac gaatacatca gtgccatcaa 1500
ggaagaaatc agcaaggtcg tcaagatcca agaggagctt gacattgatg tgcttgtgca 1560
tggagagcca gagagaaatg acatggttga gtacttcggt gagcaattat ctggttttgc 1620
gttcactgcc aacggatggg tgcaatccta tggatcacgc tgtgtgaagc cacccattat 1680
ctacggtgat gtcagccggc cgaaccccat gactgttttc tggtccaaga tggcacagag 1740
catgacccct cgtcccatga agggaatgtt gactggtccg gtcacaatcc tcaactggtc 1800

attcgtcagg aacgaccagc ctaggtttga gacatgctac caaatagctc ttgcaatcaa 1860
aaaggaggtt gaggatcttg aggctgctgg tattcaggtg atccagatcg atgaggcagc 1920
tctaagggag ggtctgccac tacgcaagtc agagcatgca ttctacctgg actgggctgt 1980
ccactctttc aggatcacca actgcggagt ccaggacacc acccagatcc acacccacat 2040
gtgctactcc aacttcaacg acatcatcca ctccatcatc gacatggatg ccgatgtgat 2100
cacgatcgag aactcccggt ctgacgagaa gctactgtcc gtcttccgtg agggtgtgaa 2160
gtacggagct ggcattggcc ctggtgtcta cgacatccac tctcctagga ttccctccac 2220
agaggagatc gcagaccgcg tcgagaagat gctcgccgtg ttcgacacca acatcctctg 2280
ggtgaaccct gactgtggtc tcaagacacg caagtacacg gaggtcaagc ccgccctgac 2340
caacatggtc tcggccacca agctcatccg cacccagctt gccagcgcga aatgaggtcg 2400
tttgatagct ccatggtctg atagcgcgga atgagccagt tgttttgaat aatttgggtg 2460
ttacccccctg ttccatggtg ttagtgttag gttagcctct cattggtgag atacgccgtt 2520
tcaagatgtg ttctaagttt ggagtgtgtg ttttcctttg ggctatgttt ctgggggtat 2580
gtgtgtgctt tggttataaa cagaaatgaa atatgcagtc ttccaattga aaaaaaaaa 2639

<210> 2
<211> 765
<212> PRT
<213> Zea mays

<400> 2

```
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
  1               5                  10                  15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
             20                  25                  30

Asp Leu Glu Lys Val Ala Thr Asp Leu Arg Ser Ser Ile Trp Lys Gln
         35                  40                  45

Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Ser Ser Tyr
     50                  55                  60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Glu
 65                  70                  75                  80

Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly Leu Ser Thr Tyr Phe Ser
                 85                  90                  95

Met Ala Arg Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
            100                 105                 110

Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Ser Thr
        115                 120                 125

Lys Phe Thr Tyr Ala Ser His Lys Ala Val Ser Glu Tyr Lys Glu Ala
    130                 135                 140

Lys Ala Leu Gly Ile Asp Thr Val Pro Val Leu Val Gly Pro Val Ser
145                 150                 155                 160

Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
                165                 170                 175

Leu Leu Ser Leu Leu Gly Ser Ile Leu Pro Ile Tyr Lys Glu Val Val
            180                 185                 190

Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Leu Asp Glu Pro
        195                 200                 205
```

Thr Leu Val Lys Asp Leu Asp Ala His Glu Leu Ala Ala Phe Ser Ser
210 215 220

Ala Tyr Ala Glu Leu Glu Ser Ser Phe Ser Gly Leu Asn Val Leu Ile
225 230 235 240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Ser Tyr Lys Thr Leu Thr
245 250 255

Ser Leu Ser Gly Val Thr Ala Tyr Gly Phe Asp Leu Ile Arg Gly Ala
260 265 270

Lys Thr Leu Asp Leu Ile Arg Ser Ser Phe Pro Ser Gly Lys Tyr Leu
275 280 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asp Asp Leu Ala
290 295 300

Ala Ser Leu Ser Thr Leu His Ser Leu Glu Ala Val Ala Gly Lys Asp
305 310 315 320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Met His Thr Ala Val Asp
325 330 335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
340 345 350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
355 360 365

Ala Gly Gln Lys Asp Glu Val Tyr Phe Ala Ala Asn Ala Ala Ala Gln
370 375 380

Ala Ser Arg Arg Ser Ser Pro Arg Val Thr Asn Glu Glu Val Gln Lys
385 390 395 400

Ala Ala Ala Ala Leu Arg Gly Ser Asp His Arg Arg Ser Thr Thr Val
405 410 415

Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
420 425 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Thr Glu Asp Glu Tyr Ile
450 455 460

Ser Ala Ile Lys Glu Glu Ile Ser Lys Val Val Lys Ile Gln Glu Glu
465 470 475 480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
500 505 510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
515 520 525

Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Lys
530 535 540

Met Ala Gln Ser Met Thr Pro Arg Pro Met Lys Gly Met Leu Thr Gly
545 550 555 560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
565 570 575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Lys Glu Val Glu
580 585 590

Asp Leu Glu Ala Ala Gly Ile Gln Val Ile Gln Ile Asp Glu Ala Ala
595 600 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ser Glu His Ala Phe Tyr Leu
610 615 620

Asp Trp Ala Val His Ser Phe Arg Ile Thr Asn Cys Gly Val Gln Asp
625 630 635 640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
645 650 655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
660 665 670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
675 680 685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Glu Lys Met Leu Ala
705 710 715 720

Val Phe Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
725 730 735

Thr Arg Lys Tyr Thr Glu Val Lys Pro Ala Leu Thr Asn Met Val Ser
740 745 750

Ala Thr Lys Leu Ile Arg Thr Gln Leu Ala Ser Ala Lys
755 760 765

<210> 3
<211> 2443
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (460)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (2398)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (2442)
<223> n = A, C, G, or T

<400> 3
ccctcagaag cgaagaagaa gccacagaga accagtctcc tactctctct cacccacaag 60
aaaaatggca tctcacatcg ttggataccc ccgcatgggt cccaagagag agctcaagtt 120
cgctctcgag tctttctggg atggcaagag cagcgccgag gatttgcaga aggtggctgc 180
tgatctcagg tcatccatct ggaagcagat ggctggtgct gggatcaagt acatccccag 240
caacactttc tcgttctatg accagctgct cgacgccacc gccaccctcg gtgccgtccc 300
ccccaggtac ggctggaccg gcggcgagat tggattcgac acctacttct ccatggccag 360
aggtaatgct accgtgcctg ctatggagat gaccaagtgg ttcgacacca actaccactt 420
tattgtccct gaattgggcc ctgatgtgaa cttcacctan gcttctcaaa aggctgttga 480
tgaatacaag gaggccaagg cgcttggagt ggataccatt cccgtactcg ttggccctgt 540
tacatacttg ttgctctcca agcctgccaa gggagtcgag aaatcctttt ctctcctctc 600
tctccttccc aaggttcttg ctgtctacaa ggaagttatt gctgacctta aggcagctgg 660
tgcttcatgg attcaatttg atgagcctac ccttgtcttg gaccttgaat ctcacaagtt 720
gcaagctttc actgacgcat atgcagaact tgcacctgct ttgtctgatc tgaatgttct 780
tgttgagacc tactttgctg acatccctgc tgaggcgtac aagaccctca catctctgaa 840
tggcgtcact gcatatgggt ttgatttggt ccgtggaacc catactcttg atttgatcaa 900
gggtggattt cccagtggaa aatacctctt tgctggagtg gttgatggaa ggaacatctg 960
ggccaatgac cttgctgctt ctctcactac attgcagggt cttgagggca ttgtgggcaa 1020
agataagctt gttgtgtcca cctcctcctc ccttcttcac actgctgttg atcttgttaa 1080
cgagaccaag ttggatgacg agatcaagtc atggctagca tttgctgcac aaaaaattgt 1140
tgaagttaac gcattggcta aggcattgtc tggcaacaag gatgtggcct tcttctctgc 1200
taatgctgca gctcaggctt caaggaagtc ctctccaaga gtgaccaacg aggctgttca 1260
gaaggctgct gctgcattga agggttcaga tcatcgccgt gcaacaaatg tcagtgccag 1320
actggatgct caacaaaaga agctcaacct tccaatcctt ccaaccacca ctattggatc 1380
cttccctcag actgtagaac tgaggagggt acgccgtgag ttcaaggcta acaagatctc 1440
cgaggaagag tatgttaagt caattaagga ggaaattcgc aaagttgttg aacttcaaga 1500
agagcttgat attgatgttc ttgttcatgg agaaccagag agaaatgata tggttgagta 1560
cttcggtgag caattgtcag gctttgcctt cactgttaat gggtgggtgc aatcctatgg 1620
ttcccgttgt gtgaagccac caatcatcta tggtgatgtg agccgcccaa agccaatgac 1680
tgtcttctgg tcatctctgg ctcagagctt taccaagcgc ccaatgaagg gaatgcttac 1740
cggtcctgtt accattctca actggtcctt tgttagaaat gaccaaccta gatctgagac 1800
cacctaccag attgctttgg ctatcaagga cgaagtggag gaccttgaaa aggctggcat 1860
cactgttatc caaattgatg aagctgcttt gagagagggt ctgccactga ggaaatcaga 1920
acaagctcac tacttggact gggctgtcca tgccttcaga atcaccaatg ttggtgtgca 1980
ggataccact cagatccaca cccacatgtg ctactccaac ttcaacgaca tcatccactc 2040
catcatcgac atggacgctg atgttatcac cattgagaac tctcgctccg atgagaagct 2100
cctgtcagtc ttccgtgaag gtgtgaagta tggtgctgga attggccctg gtgtctatga 2160
catccactcc ccaagaatac caccaactga agaaatcgct gacagaatca ataagatgct 2220
tgcagtgctc gagaagaaca tcttgtgggt caaccctgac tgtggtctca agacccgcaa 2280
gtacactgaa gtgaagccgc cctcacaaaa catggttgcc gcagcaaaac tcatccgtta 2340
cgaacttgcc aagtgaatgg tataagaaag tagaatctac aagttcaatg ggtccgcntt 2400
taaaatacac caaagaaaaa ttttcaaaat gggttgttca ana 2443

<210> 4
<211> 763
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (132)
<223> Xaa = any amino acid

<400> 4

```
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
 1               5                  10                  15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
            20                  25                  30

Asp Leu Gln Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
        35                  40                  45

Met Ala Gly Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Phe
    50                  55                  60

Tyr Asp Gln Leu Leu Asp Ala Thr Ala Thr Leu Gly Ala Val Pro Pro
65                  70                  75                  80

Arg Tyr Gly Trp Thr Gly Gly Glu Ile Gly Phe Asp Thr Tyr Phe Ser
                85                  90                  95

Met Ala Arg Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
            100                 105                 110

Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
        115                 120                 125

Asn Phe Thr Xaa Ala Ser Gln Lys Ala Val Asp Glu Tyr Lys Glu Ala
    130                 135                 140

Lys Ala Leu Gly Val Asp Thr Ile Pro Val Leu Val Gly Pro Val Thr
145                 150                 155                 160

Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
                165                 170                 175

Leu Leu Ser Leu Leu Pro Lys Val Leu Ala Val Tyr Lys Glu Val Ile
            180                 185                 190

Ala Asp Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
        195                 200                 205

Thr Leu Val Leu Asp Leu Glu Ser His Lys Leu Gln Ala Phe Thr Asp
    210                 215                 220

Ala Tyr Ala Glu Leu Ala Pro Ala Leu Ser Asp Leu Asn Val Leu Val
225                 230                 235                 240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Ala Tyr Lys Thr Leu Thr
                245                 250                 255

Ser Leu Asn Gly Val Thr Ala Tyr Gly Phe Asp Leu Val Arg Gly Thr
            260                 265                 270

His Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
        275                 280                 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
    290                 295                 300

Ala Ser Leu Thr Thr Leu Gln Gly Leu Glu Gly Ile Val Gly Lys Asp
305                 310                 315                 320
```

Lys Leu Val Val Ser Thr Ser Ser Ser Leu Leu His Thr Ala Val Asp
325 330 335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
340 345 350

Phe Ala Ala Gln Lys Ile Val Glu Val Asn Ala Leu Ala Lys Ala Leu
355 360 365

Ser Gly Asn Lys Asp Val Ala Phe Phe Ser Ala Asn Ala Ala Ala Gln
370 375 380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Glu Ala Val Gln Lys
385 390 395 400

Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
405 410 415

Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Ile Leu
420 425 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Phe Lys Ala Asn Lys Ile Ser Glu Glu Glu Tyr Val
450 455 460

Lys Ser Ile Lys Glu Glu Ile Arg Lys Val Val Glu Leu Gln Glu Glu
465 470 475 480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Val Asn
500 505 510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
515 520 525

Tyr Gly Asp Val Ser Arg Pro Lys Pro Met Thr Val Phe Trp Ser Ser
530 535 540

Leu Ala Gln Ser Phe Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545 550 555 560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
565 570 575

Ser Glu Thr Thr Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
580 585 590

Asp Leu Glu Lys Ala Gly Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
595 600 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ser Glu Gln Ala His Tyr Leu
610 615 620

Asp Trp Ala Val His Ala Phe Arg Ile Thr Asn Val Gly Val Gln Asp
625 630 635 640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
645 650 655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
660 665 670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
675 680 685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Pro Thr Glu Glu Ile Ala Asp Arg Ile Asn Lys Met Leu Ala
705 710 715 720

Val Leu Glu Lys Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
725 730 735

Thr Arg Lys Tyr Thr Glu Val Lys Pro Pro Ser Gln Asn Met Val Ala
740 745 750

Ala Ala Lys Leu Ile Arg Tyr Glu Leu Ala Lys
755 760

<210> 5
<211> 2296
<212> DNA
<213> Nicotiana plumbaginifolia

<400> 5
atggcatctc acattgttgg atatccccgt atgggcccaa agagagagct gaaatttgct 60
ctcgagtctt tctgggatgg gaagaggcgc tgaggacttg aagaaggtgg ctgcagacct 120
aaggtcttcc atctggaaac agatggctga tgctggcatc aagtacatcc ccagcaacac 180
attctcttac tatgatcagg tgcttgacac aactgcaatg ctcggtgctg tcccggctag 240
gtacaattgg gctggtggtg agatagcatt tgacacttac ttctccatgg ccagaggaaa 300
tgcctctgtc cctgctatgg agatgaccaa gtggtttgac accaactacc acttcattgt 360
ccctgagttg ggacctgatg ttaacttttc ttatgcttct cacaaggcag tagatgagta 420
caaagaggcc aaggggcttg gtgtagacac ggttccagtc cttattggtc cagtctcata 480
cttgttgcta tccaaacctg ctaagggtgt tgagaaatcc ttccctcttt tgtcacttct 540
tgacaaagtc cttccaatct acaaggaagt tattgcagaa ttgaaggctg ctggtgcttc 600
ttggattcag tttgatgaac ctacacttgt gttggatctc caagctcacc aattggaagc 660
cttcactaag gcctatgccg agttggaatc atctctgtct ggtcttaatg ttctcactga 720
aacctacttc gctgacgtcc ctgctgaagc attcaaaacc ctcactgctt tgaagggagt 780
tactgccttt ggttttgact tggttcgtgg agctcagacc cttgatttga tcaaaggtgg 840
cttcccttca ggcaagtact tgtttgctgg agtggtcgac ggaaggaaca tctgggcaaa 900
tgatcttgcc gcatctctta acctcctgca atctcttgag ggtattgttg gaaaagacaa 960
actagttgtc tccacatctt gctcacttct tcatactgct gttgatcttg tcaatgagac 1020
taagctagat gatgaaatca agtcatggtt ggcgtttgct gcccaaaaag tagttgaagt 1080
taacgctttg gccaaggcat tggctggtca caaggatgag gcattcttct ctgcaaatgc 1140
taccgctcag gcttccagga aatcctctcc aagagtgaca aatgaagctg tccaaaaggc 1200
tgctgctgca cttaagggtt ctgaccaccg ccgtgctaca aatgtcagtt ctagacttga 1260
tgcccaacaa aagaaactta acctcccagt tctcccaaca accaccattg ggtccttccc 1320
tcagacagtg gagcttagga gagttcgccg tgaatacaag gccaagaaga tctctgagga 1380
agagtatgtt aaggccatca aggcagaaat caagaaggtc gttgatctcc aggaagagct 1440
cgacatcgat gtcttggttc acggagagcc agagaggaat gatatggttg aatacttcgg 1500
agagcagctt tctggttttg ccttcactgc taatggatgg gttcaatctt atggatctcg 1560
atgtgtgaag ccaccaatta tctatggtga tgtgagccgc cccaacccaa tgactgtatt 1620
ctggtccaaa acagctcaga gcatgaccaa gcgcccaatg aagggaatgc ttaccgggcc 1680
agttaccatt ctcaactggt cttttgtcag aaatgaccag ccaagatttg aaacttgcta 1740
ccagattgct ttggccatta aggatgaagt ggaagatttg gagaaggcag gcatcactgt 1800

tatccaaatt gatgaagctg ctttgagaga ggggttgcct ctaaggaagg ctgagcacgc 1860
tttttacttg aactgggctg tccactcctt cagaatcacc aacgtcggca ttcaagacac 1920
cacccagatc cacacacaca tgtgctactc caacttcaat gacattatcc actctatcat 1980
tgacatggat gctgatgtga tcacaattga gaactcacgg tccgatgaga agctcctctc 2040
agttttcagg gagggagtta agtatggtgc tggaattggc cctggtgtct atgacatcca 2100
ctcccctaga ataccatcaa cggaagagat tgctgacaga gttaacaaga tgcttgctgt 2160
tcttgacacc aacatcttgt gggtcaaccc agattgtggt ctcaagactc gcaagtacgc 2220
tgaggtaaag ccagccctcg agaacatggt ttctgctgcc aaggccatcc gcacccaact 2280
tgccagctcc aagtga 2296

<210> 6
<211> 765
<212> PRT
<213> Nicotiana plumbaginifolia

<400> 6
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
1 5 10 15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
20 25 30

Asp Leu Lys Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
35 40 45

Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
50 55 60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Ala
65 70 75 80

Arg Tyr Asn Trp Ala Gly Gly Glu Ile Ala Phe Asp Thr Tyr Phe Ser
85 90 95

Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
100 105 110

Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
115 120 125

Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asp Glu Tyr Lys Glu Ala
130 135 140

Lys Gly Leu Gly Val Asp Thr Val Pro Val Leu Ile Gly Pro Val Ser
145 150 155 160

Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Pro
165 170 175

Leu Leu Ser Leu Leu Asp Lys Val Leu Pro Ile Tyr Lys Glu Val Ile
180 185 190

Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
195 200 205

Thr Leu Val Leu Asp Leu Gln Ala His Gln Leu Glu Ala Phe Thr Lys
210 215 220

Ala Tyr Ala Glu Leu Glu Ser Ser Leu Ser Gly Leu Asn Val Leu Thr
225 230 235 240

Glu Thr Tyr Phe Ala Asp Val Pro Ala Glu Ala Phe Lys Thr Leu Thr
245 250 255

Ala Leu Lys Gly Val Thr Ala Phe Gly Phe Asp Leu Val Arg Gly Ala
260 265 270

Gln Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
275 280 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
290 295 300

Ala Ser Leu Asn Leu Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
305 310 315 320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
325 330 335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
340 345 350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
355 360 365

Ala Gly His Lys Asp Glu Ala Phe Phe Ser Ala Asn Ala Thr Ala Gln
370 375 380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Glu Ala Val Gln Lys
385 390 395 400

Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
405 410 415

Ser Ser Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
420 425 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Glu Glu Tyr Val
450 455 460

Lys Ala Ile Lys Ala Glu Ile Lys Lys Val Val Asp Leu Gln Glu Glu
465 470 475 480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
500 505 510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
515 520 525

Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Lys
530 535 540

Thr Ala Gln Ser Met Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545 550 555 560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
565 570 575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
580 585 590

Asp Leu Glu Lys Ala Gly Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
595 600 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ala Glu His Ala Phe Tyr Leu
610 615 620

Asn Trp Ala Val His Ser Phe Arg Ile Thr Asn Val Gly Ile Gln Asp
625 630 635 640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
645 650 655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
660 665 670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
675 680 685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Asn Lys Met Leu Ala
705 710 715 720

Val Leu Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
725 730 735

Thr Arg Lys Tyr Ala Glu Val Lys Pro Ala Leu Glu Asn Met Val Ser
740 745 750

Ala Ala Lys Ala Ile Arg Thr Gln Leu Ala Ser Ser Lys
755 760 765

<210> 7
<211> 475
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (344)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (367)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (433)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (452)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (473)..(474)
<223> n = A, C, G, or T

<400> 7
cgccatcctc ctcctctccc cctatcgtct tcctccccat ctccggcgcc gctccgcgac 60
tcctccaagg aaagatggca tcccacattg ttggataccc tcgcatgggc cccaagaggg 120
agctcaagtt tgccttggag tctttctggg atgggaagag cagcgctgag gatttggaga 180
aggttgccgc cgacctcagg gccagcatct ggaagcagat gtcagaggct gggattaagt 240
acattcccag caacaccttc tcatactatg accaggtgct tgacacaacg gccatgcttg 300
gtgccgtccc ggaccgctac tcatggactg gcggagagat tggncacagc acctacttct 360
caatggncaa gggcaatgcc actgtccctg ctatggagat gaccaagtgg tttgacacca 420
actaacactt cantgtgcct gaattgagcc ancaaccaag ttctcatatg ctnna 475

<210> 8
<211> 124
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (98)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (117)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (120)
<223> Xaa = any amino acid

<400> 8
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
1 5 10 15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
20 25 30

Asp Leu Glu Lys Val Ala Ala Asp Leu Arg Ala Ser Ile Trp Lys Gln
35 40 45

Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
50 55 60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Asp
65 70 75 80

Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly His Ser Thr Tyr Phe Ser
85 90 95

Met Xaa Lys Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
100 105 110

Phe Asp Thr Asn Xaa His Phe Xaa Val Pro Glu Leu
115 120

<210> 9
<211> 628
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (219)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (254)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (300)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (319)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (331)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (335)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (338)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (348)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (350)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (360)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (413)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (416)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (424)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (428)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (440)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (455)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (469)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (473)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (484)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (504)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (506)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (526)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (533)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (535)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (552)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (568)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (580)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (598)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (600)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (606)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (613)
<223> n = A, C, G, or T

<400> 9
ggtcgtcacc cagagtgaac aattaggagg ttcagaaggc tgcggctgct ttgaagggct 60
ctgaccaccg ccgtgctacc cctgtctctg ctagactgga cgctcagcag aagaagctca 120
accttcctat cctcccaaca acaacaattg gttcattccc tcagacaatg gacctcagga 180
gggtccgccg tgagtacaag gcgaaagaag atctctgang aggagtatgt cagtgctatc 240
aaggaagaaa ttancaaagg ttgtcaagat tcaaagagga gcttgacatt gatgttctcn 300
tccaatggag aagcctgana aaaatgacat nggtnaanta cttcggcnan caaattatcn 360
gggtttgcaa ttactgccaa tggatgggtg caatcctatg gattacttgc gtnaancacc 420
gatnatcnat gggatgtaan cgcccaaccc atganatctt ctggtcaana tgntcaggac 480
atancctccc ccaatgaagg aatntnacgg cctttaaatc ccaacnggct ttntnagaac 540
acaaccaggt tnagaatgca caaattcnct gccataaaan gagttaggtt ccagctgngn 600
atcagngtca atnatagggg ccaaaagg 628

<210> 10
<211> 118
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (8)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (72)..(73)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (84)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (100)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (106)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (110)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (112)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (116)
<223> Xaa = any amino acid

<400> 10

```
Ser Ser Pro Arg Val Asn Asn Xaa Glu Val Gln Lys Ala Ala Ala Ala
  1               5                  10                  15

Leu Lys Gly Ser Asp His Arg Arg Ala Thr Pro Val Ser Ala Arg Leu
            20                  25                  30

Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Ile Leu Pro Thr Thr Thr
        35                  40                  45

Ile Gly Ser Phe Pro Gln Thr Met Asp Leu Arg Arg Val Arg Arg Glu
    50                  55                  60

Tyr Lys Ala Lys Glu Asp Leu Xaa Xaa Gly Val Cys Gln Cys Tyr Gln
65                  70                  75                  80
```

Gly Arg Asn Xaa Gln Arg Leu Ser Arg Phe Lys Glu Glu Leu Asp Ile
85 90 95

Asp Val Leu Xaa Gln Trp Arg Ser Leu Xaa Lys Met Thr Xaa Val Xaa
100 105 110

Tyr Phe Gly Xaa Gln Ile
115

<210> 11
<211> 765
<212> PRT
<213> Catharanthus roseus

<400> 11
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
1 5 10 15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Lys Lys Ser Ser Ala Glu
20 25 30

Asp Leu Gln Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
35 40 45

Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
50 55 60

Tyr Asp Gln Val Leu Asp Thr Ala Thr Met Leu Gly Ala Val Pro Pro
65 70 75 80

Arg Tyr Asn Phe Ala Gly Gly Glu Ile Gly Phe Asp Thr Tyr Phe Ser
85 90 95

Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
100 105 110

Phe Asp Thr Asn Tyr His Tyr Ile Val Pro Glu Leu Gly Pro Glu Val
115 120 125

Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asn Glu Tyr Lys Glu Ala
130 135 140

Lys Glu Leu Gly Val Asp Thr Val Pro Val Leu Val Gly Pro Val Thr
145 150 155 160

Phe Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Thr Phe Pro
165 170 175

Leu Leu Ser Leu Leu Asp Lys Ile Leu Pro Val Tyr Lys Glu Val Ile
180 185 190

Gly Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
195 200 205

Thr Leu Val Leu Asp Leu Glu Ser His Gln Leu Glu Ala Phe Thr Lys
210 215 220

Ala Tyr Ser Glu Leu Glu Ser Thr Leu Ser Gly Leu Asn Val Ile Val
225 230 235 240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Thr Tyr Lys Ile Leu Thr
245 250 255

Ala Leu Lys Gly Val Thr Gly Phe Gly Phe Asp Leu Val Arg Gly Ala
260 265 270

Lys Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
275 280 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
290 295 300

Ala Ser Leu Ser Thr Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
305 310 315 320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
325 330 335

Leu Val Asn Glu Pro Lys Leu Asp Lys Glu Ile Lys Ser Trp Leu Ala
340 345 350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
355 360 365

Ala Gly Glu Lys Asp Glu Ala Phe Phe Ser Glu Asn Ala Ala Ala Gln
370 375 380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Gln Ala Val Gln Lys
385 390 395 400

Ala Ala Ala Ala Leu Arg Gly Ser Asp His Arg Arg Ala Thr Thr Val
405 410 415

Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
420 425 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Leu Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Asp Asp Tyr Val
450 455 460

Lys Ala Ile Lys Glu Glu Ile Ser Lys Val Val Lys Leu Gln Glu Glu
465 470 475 480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
500 505 510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
515 520 525

Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Gln
530 535 540

Thr Ala Gln Ser Met Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545 550 555 560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
565 570 575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
580 585 590

Asp Leu Glu Lys Ala Gly Ile Asn Val Ile Gln Ile Asp Glu Ala Ala
595 600 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ala Glu His Ala Phe Tyr Leu
610 615 620

Asp Trp Ala Val His Ser Phe Arg Ile Thr Asn Leu Pro Leu Gln Asp
625 630 635 640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
645 650 655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Met Thr Ile Glu Asn
660 665 670

Ser Arg Ser Ser Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
675 680 685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Ile Asn Lys Met Leu Ala
705 710 715 720

Val Leu Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
725 730 735

Thr Arg Lys Tyr Ala Glu Val Lys Pro Ala Leu Glu Asn Met Val Ser
740 745 750

Ala Ala Lys Leu Ile Arg Thr Gln Leu Ala Ser Ala Lys
755 760 765

<210> 12
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12
atccaacaat gtgagatgtc atgaattctg ac 32

<210> 13
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13
gtcagaattc atgacatctc acattgttgg at 32

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14
ctcacggtcc gatgagaagc tcct 24

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15
gatcggtacc tcacttggag ctggcaagtt g 31

<210> 16
<211> 1638
<212> DNA
<213> Zea mays

<400> 16
gaattccggc tcgaagccgc cgcgaccgaa cgagcgaagc gtcccttccc gcgccgacgc 60
cgaaacccta gctcctctta cgccatggcc accgtgtcgc tcactccgca ggcggtcttc 120
tccaccgagt ccggcggcgc cctggcctct gccaccatcc tccgcttccc gccaaacttc 180
gtccgcctcc gcggcggcgg atgtcagcgc aattcctaac gctaaggttg cgcagccgtc 240
cgccgtcgta ttggccgagc gtaacctgct cggctccgac gccagcctcg ccgtccacgc 300
gggggagagg ctgggaagaa ggatagccac ggatgctatc accacgccgg tagtgaacac 360
gtcggcctac tggttcaaca actcgcaaga gctaatcgac tttaaggagg ggaggcatgc 420
tagcttcgag tatgggaggt atgggaaccc gaccacggag gcattagaga agaagatgag 480
cgcactggag aaagcagagt ccaccgtgtt tgtggcgtca gggatgtatg cagctgtggc 540
tatgctcagc gcacttgtcc ctgctggtgg gcacattgtg accaccacgg attgctaccg 600
caagacaagg atttacatgg aaaatgagct ccctaagagg ggaatttcga tgactgtcat 660
taggcctgct gacatggatg ctctccaaaa tgccttggac aacaataatg tatctctttt 720
cttcacggag actcctacaa atccatttct cagatgcatt gatattgaac atgtatcaaa 780
tatgtgccat agcaagggag cgttgctttg tattgacagt actttcgcgt cacctatcaa 840
tcagaaggca ttaactttag gtgctgacct agttattcat tctgcaacga agtacattgc 900
tggacacaat gatgttattg gaggatgcgt cagtggcaga gatgagttag tttccaaagt 960
tcgtatttac caccatgtag ttggtggtgt tctaaacccg aatgctgcgt accttatcct 1020
tcgaggtatg aagacactgc atctccgtgt gcaatgtcag aacgacactg ctcttcggat 1080
ggcccagttt ttagaggagc atccaaagat tgctcgtgtc tactatcctg gcttgccaag 1140
tcaccctgaa catcacattg ccaagagtca aatgactggc tttggcggtg ttgttagttt 1200
tgaggttgct ggagactttg atgctacgag gaaattcatt gattctgtta aaatacccta 1260
tcatgcgcct tcttttggag gctgtgagag cataattgat cagcctgcca tcatgtccta 1320
ctgggattca aaggagcagc gggacatcta cgggatcaag gacaacctga tcaggttcag 1380
cattggtgtg gaggatttcg aggatcttaa gaacgatctc gtgcaggccc tcgagaagat 1440
ctaagcactc taatcagttt gtattgacaa aatatgaggt gatggctgtc ttggatcttg 1500
tcaagatctg tgacaatgat atgagctgat gactgcgaat aagttctctt ttgcttattt 1560
tatccgtcaa attcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
aaaaaaaaaa aactcgag 1638

<210> 17
<211> 480
<212> PRT
<213> Zea mays

<400> 17

```
Asn Ser Gly Ser Lys Pro Pro Arg Pro Asn Glu Arg Ser Val Pro Ser
  1               5                  10                  15

Arg Ala Asp Ala Glu Thr Leu Ala Pro Leu Thr Pro Trp Pro Pro Cys
             20                  25                  30

Arg Ser Leu Arg Arg Arg Ser Ser Pro Pro Ser Pro Ala Ala Pro Trp
         35                  40                  45

Pro Leu Pro Pro Ser Ser Ala Ser Arg Gln Thr Ser Ser Ala Ser Ala
     50                  55                  60

Ala Ala Asp Val Ser Ala Ile Pro Asn Ala Lys Val Ala Gln Pro Ser
 65                  70                  75                  80

Ala Val Val Leu Ala Glu Arg Asn Leu Leu Gly Ser Asp Ala Ser Leu
                 85                  90                  95

Ala Val His Ala Gly Glu Arg Leu Gly Arg Arg Ile Ala Thr Asp Ala
            100                 105                 110

Ile Thr Thr Pro Val Val Asn Thr Ser Ala Tyr Trp Phe Asn Asn Ser
        115                 120                 125

Gln Glu Leu Ile Asp Phe Lys Glu Gly Arg His Ala Ser Phe Glu Tyr
    130                 135                 140

Gly Arg Tyr Gly Asn Pro Thr Thr Glu Ala Leu Glu Lys Lys Met Ser
145                 150                 155                 160

Ala Leu Glu Lys Ala Glu Ser Thr Val Phe Val Ala Ser Gly Met Tyr
                165                 170                 175

Ala Ala Val Ala Met Leu Ser Ala Leu Val Pro Ala Gly Gly His Ile
            180                 185                 190

Val Thr Thr Thr Asp Cys Tyr Arg Lys Thr Arg Ile Tyr Met Glu Asn
        195                 200                 205

Glu Leu Pro Lys Arg Gly Ile Ser Met Thr Val Ile Arg Pro Ala Asp
    210                 215                 220

Met Asp Ala Leu Gln Asn Ala Leu Asp Asn Asn Asn Val Ser Leu Phe
225                 230                 235                 240

Phe Thr Glu Thr Pro Thr Asn Pro Phe Leu Arg Cys Ile Asp Ile Glu
                245                 250                 255

His Val Ser Asn Met Cys His Ser Lys Gly Ala Leu Leu Cys Ile Asp
            260                 265                 270

Ser Thr Phe Ala Ser Pro Ile Asn Gln Lys Ala Leu Thr Leu Gly Ala
        275                 280                 285
```

Asp Leu Val Ile His Ser Ala Thr Lys Tyr Ile Ala Gly His Asn Asp
290 295 300

Val Ile Gly Gly Cys Val Ser Gly Arg Asp Glu Leu Val Ser Lys Val
305 310 315 320

Arg Ile Tyr His His Val Val Gly Gly Val Leu Asn Pro Asn Ala Ala
325 330 335

Tyr Leu Ile Leu Arg Gly Met Lys Thr Leu His Leu Arg Val Gln Cys
340 345 350

Gln Asn Asp Thr Ala Leu Arg Met Ala Gln Phe Leu Glu Glu His Pro
355 360 365

Lys Ile Ala Arg Val Tyr Tyr Pro Gly Leu Pro Ser His Pro Glu His
370 375 380

His Ile Ala Lys Ser Gln Met Thr Gly Phe Gly Gly Val Val Ser Phe
385 390 395 400

Glu Val Ala Gly Asp Phe Asp Ala Thr Arg Lys Phe Ile Asp Ser Val
405 410 415

Lys Ile Pro Tyr His Ala Pro Ser Phe Gly Gly Cys Glu Ser Ile Ile
420 425 430

Asp Gln Pro Ala Ile Met Ser Tyr Trp Asp Ser Lys Glu Gln Arg Asp
435 440 445

Ile Tyr Gly Ile Lys Asp Asn Leu Ile Arg Phe Ser Ile Gly Val Glu
450 455 460

Asp Phe Glu Asp Leu Lys Asn Asp Leu Val Gln Ala Leu Glu Lys Ile
465 470 475 480

<210> 18
<211> 3639
<212> DNA
<213> Zea mays

<400> 18
tctagattac ataatacacc taataatctt gtgttgtttg tttacttctc aacttattta 60
agttggatta tattccatct tttctttttt atttgtctgt tttagttaaa aatgaactaa 120
caaacgacaa atattcgaga acgagatagt ataatctata ggataatcag acatgtcctt 180
agagggtgtt tgtttagaat tataatatgt atagaatata taatccaaca aattttgaac 240
taacaagttt aaaatttgat agattatata atctgggcac attataatcc taaacaaaca 300
ccatcttagt aatttttat ttagtgctcc gtttggatgt gaagaagatg gagttgaata 360
ccaaatcatg tatgatactg aaatgagatg taattttaat tctattgttt ggatgtcgtt 420
gaattggagt ttgaagttat gcggtctaat tttacgcaat accgagatga gactttatac 480
taggagaggg gtttctagtt atagcctaat tctaaagaat tgagtctcta tttccaaatc 540
ttaattttat gcaactaaac aacacaattt agaaaaactg ttttcaattt cttattctgt 600
gctccaaacg aggtggagta tttagaagta gataagcgcc tctgctgcac gaagcgatga 660
acgcactctg acggtcttgc cactacaaat aagccgcacc gcatttcgga aggccacgcg 720
accgccacct ccccgaagct gccgcgaccg atcgagcgaa gcgtcgctcc ccgcgccgcc 780
gccaaaaccc tagcttctcc tactccatgg ccactgtctc gctcaccccg caggctgtct 840
tctccacgga gtccggtggc gccctggcct ctgctaccat cctccgcttt ccgccaaact 900
ttgtccgcca gcttagcacc aaggcacgcc gcaactgcag caacatcggc gtcgcgcaga 960
tcgtcgccgc cgcgtggtcc gactgccccg ccgctcgccc ccacttaggc ggcggcggcc 1020
gccgcgcccg cggcgtggcc tcctcccacg ccgcggctgc atcggccgcc gccgccgcct 1080

ccgcggcggc ggaggtcagc gcaattccca acgctaaggt tgcgcaaccg tccgccgtcg 1140
tcttggccga gcgtaacctg ctcggctccg acgccagcct cgccgtccac gcgggtaccc 1200
taccctgcta gctcgtctct ttactgtaag atctaggttc tatgcttttt tccccttcg 1260
atgattcctt tgtggctttg ctgccttttt atctgaaaca ggggagaggc tgggaagaag 1320
gatcgccacg gatgcgatca ccacaccggt agtgaacacg tcggcctact ggttcaacaa 1380
ctcgcaagag ctaatcgact ttaaggtagt gaatattcgt gcttgctctt gtctaatttg 1440
acggatgtga gttttgacgc cgaaatatta agttttatct gttccttagg aggggaggca 1500
tgctagcttc gagtatggga ggtatgggaa cccgaccacg gaggcattag agaagaagat 1560
gaggtgatgc tcgatagtgg aaatgtcggc accctgttgg ttgcatttgg ctggaggcta 1620
aacagttgcg tgttctcatg gtgcagcgca ctggagaaag cagagtccac agtgttcgtg 1680
gcatcgggga tgtatgcagc tgcggctatg ctcagtgcac ttgttccggc tggtgggcac 1740
attgtgacca ccacggattg ctaccggaaa acaaggattt acatggaaac tgagctcccc 1800
aagaggggaa tttcggtaat accatgcgat cttttaagct ctacttgttt ttagaacggg 1860
acatctgcta tcactattgg ttgtcttcct gtcactgtgc tacagtagtg ggtctacaat 1920
gaacttgctc ttattcagtt aaaattactc tgtcgtgttg tccttatcta gctaatagtc 1980
tctacaaagt tcagttactt cagcatagcc aataggagta gcataactac tgcagggtat 2040
atgaacaata tcctttgcag tagctgttgg gagtacacag tacagtatgg cttcagactt 2100
tattctttgt actgcattgg gtgaagccac atagggtttg ccgagtgcac gtgcaccagg 2160
gaaaaaacaa tttctacttt tctagtgatt aaaaactaaa ttttaccact catgcacacc 2220
ctaattttta attagagaag attttcaata catgtgtata ttgaaatgtc aagtgtgcac 2280
tcggattctc cggcctctag cttcgcccga ctgcaatgtc aataggattg gctatctgta 2340
aaggatttaa gtagaactgc ttgtggtaat aaattttagg atccctcaca ataagattta 2400
ttatataatc acaccatcta ccagttgaaa tgcagtgaga gcactttgtg agttgtatac 2460
caatgtttct cacgcttcac ttagcatgtg atactgttta tgctcagatg actgtcatta 2520
ggcctgctga catggatgct ctacaaaatg cgttggacaa caataatgtg agtgtggtat 2580
catttccatt gcccctgatc gtggtaaaaa acatacatta atacatttgc aaatgtagcc 2640
taaccttatg gccatgtcag gtatctcttt tcttcacgga gactcccaca aatccatttc 2700
tcagatgcat tgatattgaa catgtatcaa atatgtgcca tagcaaggga gcgttgcttt 2760
gtatcgacag tacttttgcc tcccctatca atcagaaggc actgacttta ggcgctgacc 2820
tagttattca ttctgcaaca aagtacattg ctggacacaa cgatgtgagt tgatatactg 2880
aaccccatct cccctcatta aagttatgtg tttgcacatt gcactaacta gtacttcaac 2940
ttcccaggtt attggaggat gcgtcagtgg cagagatgag ttggtttcca aagtccgtat 3000
ttatcaccat gtggttggtg gtgttctaaa cccggtaagt ttagattgtt aaagttttgt 3060
ttccatttat ttcatcttcc ttgcacaggt tgtatgtatt tacagattcc catagttaca 3120
agcttctatt tttataggta gaaaatcgtg taattttctt tagtagcata tgtttaggtt 3180
agaaaaataa tttgctttct ctgagtatca caaaccgcat ccagttctct gttacatgaa 3240
ctagaattct ggttctggaa aggaagaaat aggatatgtt ctgtgcactg caatatatat 3300
ctaatcatta atccggagct ttatgtcaca gactcacagg ccaggctacc actttatgaa 3360
atattccaaa ttatgcttgt ctcaaaatgg aatgactcat gttgtactct gttccaacgt 3420
tttcaaatca tgactaggat tctagttgcc cggacaccga ctaggtgatt aatcgtgact 3480
aggcattgac tagtcacgat tagttttgag ctagtcgaac ttatcaacaa cttgttccag 3540
gcaatatatt gcagtactat gccttattga ttgggtatat aaatgaattt tagcacacag 3600
atagagcaga agtaagacaa attaacacaa agttctaga 3639

<210> 19
<211> 509
<212> PRT
<213> Zea mays

<400> 19
Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser
1 5 10 15

Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe
20 25 30

Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly
35 40 45

Val Ala Gln Ile Val Ala Ala Ala Trp Ser Asp Cys Pro Ala Ala Arg
50 55 60

Pro His Leu Gly Gly Gly Gly Arg Arg Ala Arg Gly Val Ala Ser Ser
65 70 75 80

His Ala Ala Ala Ala Ser Ala Ala Ala Ala Ala Ser Ala Ala Ala Glu
85 90 95

Val Ser Ala Ile Pro Asn Ala Lys Val Ala Gln Pro Ser Ala Val Val
100 105 110

Leu Ala Glu Arg Asn Leu Leu Gly Ser Asp Ala Ser Leu Ala Val His
115 120 125

Ala Gly Glu Arg Leu Gly Arg Arg Ile Ala Thr Asp Ala Ile Thr Thr
130 135 140

Pro Val Val Asn Thr Ser Ala Tyr Trp Phe Asn Asn Ser Gln Glu Leu
145 150 155 160

Ile Asp Phe Lys Glu Gly Arg His Ala Ser Phe Glu Tyr Gly Arg Tyr
165 170 175

Gly Asn Pro Thr Thr Glu Ala Leu Glu Lys Lys Met Ser Ala Leu Glu
180 185 190

Lys Ala Glu Ser Thr Val Phe Val Ala Ser Gly Met Tyr Ala Ala Val
195 200 205

Ala Met Leu Ser Ala Leu Val Pro Ala Gly Gly His Ile Val Thr Thr
210 215 220

Thr Asp Cys Tyr Arg Lys Thr Arg Ile Tyr Met Glu Asn Glu Leu Pro
225 230 235 240

Lys Arg Gly Ile Ser Met Thr Val Ile Arg Pro Ala Asp Met Asp Ala
245 250 255

Leu Gln Asn Ala Leu Asp Asn Asn Asn Val Ser Leu Phe Phe Thr Glu
260 265 270

Thr Pro Thr Asn Pro Phe Leu Arg Cys Ile Asp Ile Glu His Val Ser
275 280 285

Asn Met Cys His Ser Lys Gly Ala Leu Leu Cys Ile Asp Ser Thr Phe
290 295 300

Ala Ser Pro Ile Asn Gln Lys Ala Leu Thr Leu Gly Ala Asp Leu Val
305 310 315 320

Ile His Ser Ala Thr Lys Tyr Ile Ala Gly His Asn Asp Val Ile Gly
325 330 335

Gly Cys Val Ser Gly Arg Asp Glu Leu Val Ser Lys Val Arg Ile Tyr
340 345 350

His His Val Val Gly Gly Val Leu Asn Pro Asn Ala Ala Tyr Leu Ile
355 360 365

Leu Arg Gly Met Lys Thr Leu His Leu Arg Val Gln Cys Gln Asn Asp
370 375 380

Thr Ala Leu Arg Met Ala Gln Phe Leu Glu Glu His Pro Lys Ile Ala
385 390 395 400

Arg Val Tyr Tyr Pro Gly Leu Pro Ser His Pro Glu His His Ile Ala
405 410 415

Lys Ser Gln Met Thr Gly Phe Gly Gly Val Val Ser Phe Glu Val Ala
420 425 430

Gly Asp Phe Asp Ala Thr Arg Lys Phe Ile Asp Ser Val Lys Ile Pro
435 440 445

Tyr His Ala Pro Ser Phe Gly Gly Cys Glu Ser Ile Ile Asp Gln Pro
450 455 460

Ala Ile Met Ser Tyr Trp Asp Ser Lys Glu Gln Arg Asp Ile Tyr Gly
465 470 475 480

Ile Lys Asp Asn Leu Ile Arg Phe Ser Ile Gly Val Glu Asp Phe Glu
485 490 495

Asp Leu Lys Asn Asp Leu Val Gln Ala Leu Glu Lys Ile
500 505

<210> 20
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 20
aattcatgag tgca 14

<210> 21
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21
aatttgcact catg 14

<210> 22
<211> 1350
<212> DNA
<213> Escherichia coli

<400> 22
atggctgaaa ttgttgtctc caaatttggc ggtaccagcg tagctgattt tgacgccatg 60
aaccgcagcg ctgatattgt gctttctgat gccaacgtgc gtttagttgt cctctcggct 120
tctgctggta tcactaatct gctggtcgct ttagctgaag gactggaacc tggcgagcga 180
ttcgaaaaac tcgacgctat ccgcaacatc cagtttgcca ttctggaacg tctgcgttac 240

```
ccgaacgtta tccgtgaaga gattgaacgt ctgctggaga acattactgt tctggcagaa  300
gcggcggcgc tggcaacgtc tccggcgctg acagatgagc tggtcagcca cggcgagctg  360
atgtcgaccc tgctgtttgt tgagatcctg cgcgaacgcg atgttcaggc acagtggttt  420
gatgtacgta aagtgatgcg taccaacgac cgatttggtc gtgcagagcc agatatagcc  480
gcgctggcgg aactggccgc gctgcagctg ctcccacgtc tcaatgaagg cttagtgatc  540
acccagggat ttatcggtag cgaaaataaa ggtcgtacaa cgacgcttgg ccgtggaggc  600
agcgattata cggcagcctt gctggcggag gctttacacg catctcgtgt tgatatctgg  660
accgacgtcc cgggcatcta caccaccgat ccacgcgtag tttccgcagc aaaacgcatt  720
gatgaaatcg cgtttgccga agcggcagag atggcaactt ttggtgcaaa agtactgcat  780
ccggcaacgt tgctacccgc agtacgcagc gatatcccgg tctttgtcgg ctccagcaaa  840
gacccacgcg caggtggtac gctggtgtgc aataaaactg aaaatccgcc gctgttccgc  900
gctctggcgc ttcgtcgcaa tcagactctg ctcactttgc acagcctgaa tatgctgcat  960
tctcgcggtt tcctcgcgga agttttcggc atcctcgcgc ggcataatat ttcggtagac 1020
ttaatcacca cgtcagaagt gagcgtggca ttaacccttg ataccaccgg ttcaacctcc 1080
actggcgata cgttgctgac gcaatctctg ctgatggagc tttccgcact gtgtcgggtg 1140
gaggtggaag aaggtctggc gctggtcgcg ttgattggca atgacctgtc aaaagcctgc 1200
gccgttggca aagaggtatt cggcgtactg gaaccgttca acattcgcat gatttgttat 1260
ggcgcatcca gccataacct gtgcttcctg gtgcccggcg aagatgccga gcaggtggtg 1320
caaaaactgc atagtaattt gtttgagtaa                                  1350
```

<210> 23
<211> 449
<212> PRT
<213> Escherichia coli

<400> 23

```
Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp
  1               5                  10                  15

Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn
             20                  25                  30

Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
         35                  40                  45

Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
     50                  55                  60

Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr
 65                  70                  75                  80

Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr
                 85                  90                  95

Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp
            100                 105                 110

Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
        115                 120                 125

Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys
    130                 135                 140

Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala
145                 150                 155                 160

Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu
                165                 170                 175
```

Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg
180 185 190

Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu
195 200 205

Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro
210 215 220

Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile
225 230 235 240

Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala
245 250 255

Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile
260 265 270

Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu
275 280 285

Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu
290 295 300

Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His
305 310 315 320

Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn
325 330 335

Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr
340 345 350

Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln
355 360 365

Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu
370 375 380

Gly Leu Ala Leu Val Ala Leu Ile Gly Asn Asp Leu Ser Lys Ala Cys
385 390 395 400

Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
405 410 415

Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
420 425 430

Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
435 440 445

Glu

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
gatccatggc tgaaattgtt gtctccaaat ttggcg 36

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 25
gtaccgccaa atttggagac aacaatttca gccatg 36

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 26
atggcagcca agatgcttgc attgttcgct 30

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 27
gaatgcagca ccaacaaagg gttgctgtaa 30

<210> 28
<211> 2123
<212> DNA
<213> Zea mays

<400> 28
tctagagcct attaccatct ctactcacgg gtcgtagagg tggtgaggta ggctacagct 60
ggtgacaatc ctactcaccc tttgtaatcc tctacggctc tacgcgtagt taattggtta 120
gatgtcaacc ccctctctaa gtggcagtag tgggcttggt tatacctgct agtgcctggg 180
gatgttctat ttttctagta gtgcttgatc aaacattgca tagtttgact tgggacaaac 240
tgtctgatat atatatatat ttttgggcag agggagcagt aagaacttat ttagaaatgt 300
aatcatttgt taaaaaaggt ttaattttgc tgctttcttt cgttaatgtt gttttcacat 360
tagattttct ttgtgttata tacactggat acatacaaat tcagttgcag tagtctctta 420
atccacatca gctaggcata ctttagcaaa agcaaattac acaaatctag tgtgcctgtc 480
gtcacattct caataaactc gtcatgtttt actaaaagta ccttttcgaa gcatcatatt 540
aatccgaaaa cagttaggga agtctccaaa tctgaccaaa tgccaagtca tcgtccagct 600
tatcagcatc caactttcag tttcgcatgt gctagaaatt gtttttcatc tacatggcca 660
ttgttgactg catgcatcta taaataggac ctagacgatc aatcgcaatc gcatatccac 720
tattctctag gaagcaaggg aatcacatcg ccatggcagc caagatgttt gcattgtttg 780
cgctcctagc tctttgtgca accgccacta gtgctaccca tatcccaggg cacttgtcac 840
cactactgat gccattggct accatgaacc catggatgca gtactgcatg aagcaacagg 900

gggttgccaa cttgttagcg tggccgaccc tgatgctgca gcaactgttg gcctcaccgc 960
ttcagcagtg ccagatgcca atgatgatgc cgggtatgat gccaccgatg acgatgatgc 1020
cgatgccgag tatgatgcca tcgatgatgg tgccgactat gatgtcacca atgacgatgg 1080
ctagtatgat gccgccgatg atgatgccaa gcatgatttc accaatgacg atgccgagta 1140
tgatgccttc gatgataatg ccgaccatga tgtcaccaat gattatgccg agtatgatgc 1200
caccaatgat gatgccgagc atggtgtcac caatgatgat gccaaacatg atgacagtgc 1260
cacaatgtta ctctggttct atctcacaca ttatacaaca acaacaatta ccattcatgt 1320
tcagccccac agccatggcg atcccaccca tgttcttaca gcagcccttt gttggtgctg 1380
cattctagat ctagatataa gcatttgtgt agtacccaat aatgaagtcg gcatgccatc 1440
gcatacgact cattgtttag gaataaaaca agctaataat gacttttctc tcattataac 1500
ttatatctct ccatgtctgt ttgtgtgttt gtaatgtctg ttaatcttag tagattatat 1560
tgtatatata accatgtatt ctctccattc caaattatag gtcttgcatt tcaagataaa 1620
tagttttaac catacctaga cattatgtat atataggcgg cttaacaaaa gctatgtact 1680
cagtaaaatc aaaacgactt acaatttaaa atttagaaag tacattttta ttaatagact 1740
aggtgagtac ttgtgcgttg caacgggaac atataataac ataataactt atatacaaaa 1800
tgtatcttat attgttataa aaaatatttc ataatccatt tgtaatccta gtcatacata 1860
aattttgtta ttttaattta gttgtttcac tactacattg caaccattag tatcatgcag 1920
acttcgatat atgccaagat ttgcatggtc tcatcattga agagcacatg tcacacctgc 1980
cggtagaagt tctctcgtac attgtcagtc atcaggtacg caccaccata cacgcttgct 2040
taaacaaaaa aacaagtgta tgtgtttgcg aagagaatta agacaggcag acacaaagct 2100
acccgacgat ggcgagtcgg tca 2123

<210> 29
<211> 211
<212> PRT
<213> Zea mays

<400> 29
Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
1 5 10 15

Thr Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Leu Leu
20 25 30

Met Pro Leu Ala Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln
35 40 45

Gln Gly Val Ala Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln
50 55 60

Leu Leu Ala Ser Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro
65 70 75 80

Gly Met Met Pro Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro
85 90 95

Ser Met Met Val Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met
100 105 110

Met Pro Pro Met Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro
115 120 125

Ser Met Met Pro Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile
130 135 140

Met Pro Ser Met Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro
145 150 155 160

Met Met Met Pro Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser
165 170 175

Ile Ser His Ile Ile Gln Gln Gln Leu Pro Phe Met Phe Ser Pro
180 185 190

Thr Ala Met Ala Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly
195 200 205

Ala Ala Phe
210

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 30
atgaaccctt ggatgca 17

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 31
cccacagcaa tggcgat 17

<210> 32
<211> 639
<212> DNA
<213> Zea mays

<400> 32
ccatggcagc caagatgttt gcattgtttg cgctcctagc tctttgtgca accgccacta 60
gtgctaccca tatcccaggg cacttgtcac cactactgat gccattggct accatgaacc 120
cttggatgca gtactgcatg aagcaacagg gggttgccaa cttgttagcg tggccgaccc 180
tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc 240
cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg 300
tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgccaa 360
gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga 420
tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atggtgtcac 480
caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca 540
ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atcccaccca 600
tgttcttaca gcagcccttt gttggtgctg cattctaga 639

<210> 33
<211> 211
<212> PRT
<213> Zea mays

<400> 33
Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
1 5 10 15

Thr Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Leu Leu
20 25 30

Met Pro Leu Ala Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln
35 40 45

Gln Gly Val Ala Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln
50 55 60

Leu Leu Ala Ser Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro
65 70 75 80

Gly Met Met Pro Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro
85 90 95

Ser Met Met Val Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met
100 105 110

Met Pro Pro Met Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro
115 120 125

Ser Met Met Pro Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile
130 135 140

Met Pro Ser Met Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro
145 150 155 160

Met Met Met Pro Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser
165 170 175

Ile Ser His Ile Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro
180 185 190

Thr Ala Met Ala Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly
195 200 205

Ala Ala Phe
210

<210> 34
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 34
ctagcccggg tac 13

<210> 35
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 35
ctaggtaccc ggg 13

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 36
ccacttcatg acccatatcc cagggcactt 30

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 37
ttctatctag aatgcagcac caacaaaggg 30

<210> 38
<211> 579
<212> DNA
<213> Zea mays

<400> 38
tcatgaccca tatcccaggg cacttgtcac cactactgat gccattggct accatgaacc 60
cttggatgca gtactgcatg aagcaacagg gggttgccaa cttgttagcg tggccgaccc 120
tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc 180
cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg 240
tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgccaa 300
gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga 360
tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atggtgtcac 420
caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca 480
ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atcccaccca 540
tgttcttaca gcagcccttt gttggtgctg cattctaga 579

<210> 39
<211> 191
<212> PRT
<213> Zea mays

<400> 39
Met Thr His Ile Pro Gly His Leu Ser Pro Leu Leu Met Pro Leu Ala
1 5 10 15

Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln Gln Gly Val Ala
20 25 30

Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln Leu Leu Ala Ser
35 40 45

Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro Gly Met Met Pro
50 55 60

Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro Ser Met Met Val
65 70 75 80

Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met Met Pro Pro Met
85 90 95

Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro Ser Met Met Pro
100 105 110

Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile Met Pro Ser Met
115 120 125

Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro Met Met Met Pro
130 135 140

Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser Ile Ser His Ile
145 150 155 160

Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro Thr Ala Met Ala
165 170 175

Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly Ala Ala Phe
180 185 190

<210> 40
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 40
ctagaagcct cggcaacgtc agcaacggcg gaagaatccg gtg 43

<210> 41
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 41
catgcaccgg attcttccgc cgttgctgac gttgccgagg ctt 43

<210> 42
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 42
gatcccatgg cgccccttaa gtccaccgcc agcctccccg tcgcccgccg ctcct 55

<210> 43
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 43
ctagaggagc ggcgggcgac ggggaggctg gcggtggact taaggggcgc catgg 55

<210> 44
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 44
catggcgccc accgtgatga tggcctcgtc ggccaccgcc gtcgctccgt tccaggggc 59

<210> 45
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 45
ttaagcccct ggaacggagc gacggcggtg gccgacgagg ccatcatcac ggtgggcgc 59

<210> 46
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 46
catggctggc ttccccacga ggaagaccaa caatgacatt acctccattg ctagcaacgg 60
tggaagagta caatg 75

<210> 47
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 47
catgcattgt actcttccac cgttgctagc aatggaggta atgtcattgt tggtcttcct 60
cgtggggaag ccagc 75

<210> 48
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 48
catggcttcc tcaatgatct cctccccagc tgttaccacc gtcaaccgtg ccggtgccgg 60
catggttgct ccattcaccg gcctcaaaag 90

<210> 49
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 49
catgcttttg aggccggtga atggagcaac catgccggca ccggcacggt tgacggtggt 60
aacagctggg gaggagatca ttgaggaagc 90

<210> 50
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 50
gactatccat ggcacattgt actcttccac c 31

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 51
tactaaccat ggcttcctca 20

<210> 52
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 52
ggccatggcc gc 12

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 53
gaaaccatgg ccagtgtgat tgcgcaggca 30

<210> 54
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 54
gaaaggtacc ttacaacaac tgtgccagc 29

<210> 55
<211> 1494
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1461)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (1464)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (1465)
<223> n = A, C, G, or T

<400> 55
atttgcagca caaaaagttg ttgaagtaaa tgccttggcc aaggcattgt ctggacagaa 60
ggatgaggtt ttcttttctg ctaatgctgc tgccttggct tcaaggaagt cctccccaag 120
ggtgataaat gaggctgtcc aaaaagccgc tgctgctctg aagggctctg atcatcggag 180
ggccacaaat gttagtgcca ggttggatgc tcaacagaag aaattgaatc tttctgttct 240
tccaacaact acaattggat ctttccctca aactgccgat cttagaagrg twcgycgtga 300
attcaaggct aacaagatct ccgaggaaga gtatgthaag tcaattaagg aggaaattcg 360
caaagttgtt garcttcaag aagagcttga tattgatgtt cttgttcatg gagaaccaga 420
gagaaatgat atggttgagt acttcggtga rcaattgtca ggctttgcct tcacygttaa 480
tgggtgggtg caatcctatg gttcccgttg ygtgaagcca ccratcatct atggtgatgt 540
gagccgccca aagccaatga cygtcttctg gtcatctctg gctcagagct ttaccaagcg 600
cccaatgaag ggaatgctta ccggtcctgt taccattctc aactggkcct ttgtwagaaa 660
tgaccaacct agatctgaga ccacctacca gattgctttg gctatcaagg acgaagtgga 720
ggaccttgaa aaggctggca tcactgttat ccaaattgat gaagctgctt tgagagaggg 780
tctgccactg rggaaatcag aacaagctca ctacttggac tgggctgtcc atgccttcag 840
aatcaccaat gttggtgtgc aggataccac tcagatccac acccacatgt gctactccaa 900
cttcaacgac atcatccact ccatcatcga catggacgct gatgttatca ccattgagaa 960
ctctcgctcc gatgagaagc tcctgtcagt cttccgtgaa ggtgtgaagt atggtgctgg 1020
aattgsccct ggtgtctatg acatccactc cccaagaata ccaccaactg aagaaatcgc 1080
tgacagaatc aataagatgc tggcagtgct cgagaagaac atcttgtggg tcaaccctga 1140
ctgtggtctc aagacccgca agtacactga agtgaagccc gccctcacaa acatggttgc 1200
cgcagcaaaa ctcatccgta acgaacttgc caagtgaatg gtataagaaa gtagaatcta 1260
caagttcatt ggttctgctt ttataataca ccaaagaaaa attttctata ttgggttgtt 1320
tcaataaccg tgtgtggaat atttagatgt tttagcatgc tctgtgagca attgattctt 1380
cctcaacccc tctcccctta tttttcccaa ctcctgtttt ccctaatgaa tgttgtatct 1440
ttgctttgcc gcaatcctta nttnngatat gaaatattac cagttttgtg caaa 1494